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Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-19 (Canceled).

Claim 20 (Currently amended): A method for identifying antifungal agents comprising
i. incubating, with at least one candidate compound, a fungal GTP cyclohydrolase II polypeptide under conditions allowing the binding of the candidate compound to the fungal GTP cyclohydrolase II; and

ii. selecting, by step ii), at least a candidate compound which binds to the fungal GTP cyclohydrolase II of step i); or

iii. selecting, by step iii), at least one candidate compound which reduces or blocks the activity of the fungal GTP cyclohydrolase II of step i); or

iv. selecting, by step iv), at least one candidate compound which inhibits or decreases transcription, translation or expression of the fungal GTP cyclohydrolase II of step i)[[.]]

~~wherein the GTP cyclohydrolase II activity in steps ii to iv is determined by~~

~~a) adding GTP or GTP analog, NAD⁺ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II [[or I]]; and~~

~~b) determining the NADH content.~~

Claim 21 (Previously presented): The method of claim 20, wherein the fungal GTP cyclohydrolase II is encoded by a nucleic acid sequence comprising

a) a nucleic acid sequence shown in SEQ ID No: 1; or

b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID No: 2 by back translation; or

c) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from a functional equivalent of the amino acid sequence shown in SEQ ID No: 2, which has an identity with SEQ ID No: 2 of at least 49%, by back translation.

Claim 22 (Previously presented): A nucleic acid having a sequence comprising

a) a nucleic acid sequence shown in SEQ ID No: 4; or

b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID No: 5 by back translation; or

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c) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from a functional equivalent of the amino acid sequence shown in SEQ ID No: 5, which has an identity with SEQ ID No: 5 of at least 66%, by back translation.

Claim 23 (Previously presented): The method of claim 20, wherein the method comprises testing a candidate compound in a fungal GTP cyclohydrolase II inhibition assay.

Claim 24 (Previously presented): The method of claim 23, wherein the method comprises
a) incubating, with a candidate compound, a fungal GTP cyclohydrolase II in a cell free system;

b) selecting, by step b), a candidate compound which decreases the activity of the fungal GTP cyclohydrolase II.

Claim 25 (Previously presented): The method of claim 24, wherein the enzymatic activity of the fungal GTP cyclohydrolase II is determined in comparison to the activity of a fungal GTP cyclohydrolase II not incubated with the candidate compound.

Claim 26 (Previously presented): A method for determination of GTP cyclohydrolase I or II activity comprising the steps of

- a) adding GTP or GTP analog, NAD⁺ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II or I; and
- b) determining the NADH content.

Claim 27 (Previously presented): A method for identification of inhibitors of GTP cyclohydrolase I or II comprising the following steps:

- a) adding GTP or GTP analog, NAD⁺ and formate dehydrogenase to a sample comprising GTP cyclohydrolase I or II;
- b) adding formate, NAD⁺ and formate dehydrogenase to a second sample comprising GTP cyclohydrolase I or II;
- c) adding to the sample of step a) and step b) a candidate compound;
- d) determining the activity of both samples;
- e) selecting candidate compounds that show inhibition in the presence of GTP and no inhibition in the presence of formic acid.

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Claim 28 (Previously presented): The method of claim 24, wherein inhibitors of fungal GTP cyclohydrolase II are identified in an inhibition assay comprising the following steps:

- a) adding GTP or GTP analog, NAD⁺ and formate dehydrogenase to a sample comprising GTP cyclohydrolase I or II;
- b) adding formate, NAD⁺ and formate dehydrogenase to a second sample comprising GTP cyclohydrolase I or II;
- c) adding to the sample of step a) and step b) a candidate compound;
- d) determining the activity of both samples;
- e) selecting candidate compounds that show inhibition in the presence of GTP and no inhibition in the presence of formic acid.

Claim 29 (Currently amended): The method of claim ~~[[24]]~~ 38, wherein GTP is used as substrate and the NADH content is determined by monitoring the increase in the absorption at 340nm.

Claim 30 (Previously presented): The method of claim 28, wherein GTP is used as substrate and the NADH content is determined by monitoring the increase in the absorption at 340nm.

Claim 31 (Currently amended): The method of claim ~~[[1]]~~ 20, wherein the method comprises the following steps:

- a) generating organisms which, following transformation with a nucleic acid sequence encoding GTP cyclohydrolase II are capable of overexpressing polypeptide with GTP cyclohydrolase II activity;
- b) applying to the organism of step a) and to an analogous, untransformed organism, a candidate compound;
- c) determining the growth, the viability or infectivity of the transgenic and the untransformed organism following application of the substance of step b);
- d) selecting candidate compounds, which reduces growth, viability or infectivity of the transgenic and the untransformed organism following application of the substance of step b).

Claim 32 (Previously presented): The method of claim 31, wherein the transgenic organism and the untransformed organism are fungi.

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Claim 33 (Previously presented): The method of claim 20, wherein the substances are identified in a high-throughput screening.

Claim 34 (Previously presented): The method of claim 20, wherein the antifungal agent identified via the method is applied to a phytopathogenic fungus in order to verify the fungicidal activity.

Claim 35 (Previously presented): A process for the preparation of a fungicidal composition, which comprises

- a) identifying an antifungal agent via a method for identifying antifungal agents comprising
 - i. incubating, with at least-one candidate compound, a fungal GTP cyclohydrolase II polypeptide under conditions allowing the binding of the candidate compound to the fungal GTP cyclohydrolase II; and
 - ii. selecting, by step ii), at least a candidate compound which binds to the fungal GTP cyclohydrolase II of step i) ; or
 - iii. selecting, by step iii) , at least one candidate compound which reduces or blocks the activity of the fungal GTP cyclohydrolase II of step i); or
 - iv. selecting, by step iv), at least one candidate compound which inhibits or decreases transcription, translation or expression of the fungal GTP cyclohydrolase II of step i),wherein the GTP cyclohydrolase II activity in steps ii to iv is determined by
 - 1) adding GTP or GTP analog, NAD⁺ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II or I; and
 - 2) determining the NADH content; and
- b) formulating the antifungal agent identified via (a), or an agriculturally useful salt of the active ingredient identified via (a), with suitable adjuvants.

Claim 36 (Previously presented): A process for the preparation of a pharmaceutical fungicidal composition, which comprises

- a) identifying an antifungal agent via a method for identifying antifungal agents comprising
 - i. incubating, with at least-one candidate compound, a fungal GTP cyclohydrolase II polypeptide under conditions allowing the binding of the candidate compound to the fungal GTP cyclohydrolase II; and

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- ii. selecting, by step ii), at least a candidate compound which binds to the fungal GTP cyclohydrolase II of step i) ; or
- iii. selecting, by step iii) , at least one candidate compound which reduces or blocks the activity of the fungal GTP cyclohydrolase II of step i); or
- iv. selecting, by step iv), at least one candidate compound which inhibits or decreases transcription, translation or expression of the fungal GTP cyclohydrolase II of step i),
 - wherein the GTP cyclohydrolase II activity in steps ii to iv is determined by
 - 1) adding GTP or GTP analog, NAD^+ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II or I; and
 - 2) determining the NADH content; and
- b) formulating the antifungal agent identified via (a), or a pharmaceutically useful salt of the active ingredient identified via (a), with suitable excipients.

Claim 37 (Previously presented): A method for culturing plants or plant cells or plant tissues thereby controlling fungal growth comprising treating said culture with a fungicide, wherein said fungicide is a compound which is an inhibitor of fungal GTP cyclohydrolase II.

Claim 38 (New): The method of claim 24, wherein the GTP cyclohydrolase II activity is determined by

- a) adding GTP or GTP analog, NAD^+ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II; and
- b) determining the NADH content.

Claim 39 (New): The method of claim 25, wherein the GTP cyclohydrolase II activity is determined by

- a) adding GTP or GTP analog, NAD^+ and formate dehydrogenase to a sample comprising GTP cyclohydrolase II; and
- b) determining the NADH content.